

SEQUENCE SEARCH SUMMARY

10/733, 776

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 21:08:08 ; Search time 10887 Seconds
(without alignments)
6889.747 Million cell updates/sec

Title: US-10-733-776-1
Perfect score: 1548
Sequence: 1 tcgcgatctggtactgtaag.....tgatcgggtccgaagaagatc 1548

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
	1	1548	100.0	1548	6	CQ849491	2004 Appl CQ849491 Sequence
c	2	1548	100.0	110000	1	U00096_44	2004 Y Continuation (45 o

c	3	1548	100.0	338534	1	ECOUW93	1995 Blattner	U14003 Escherichia	seq only
c	4	1532	99.0	243184	1	AP002568	2000 Genome	AP002568 Escherich	
	5	1477.6	95.5	12561	1	AE015432	Genome 2002	AE015432 Shigella	
	6	1477.6	95.5	225944	1	AE016993	"	AE016993 Shigella	
c	7	1458.4	94.2	306118	1	AE016771	"	AE016771 Escherich	
c	8	1075	69.4	13970	1	AE005657	11 2001	AE005657 Escherich	
c	9	975.6	63.0	1411	6	CQ849499	Appl 2004	CQ849499 Sequence	
	10	962.2	62.2	221961	2	AC147436	seq only	AC147436 Gallus ga	
	11	731	47.2	151040	2	AC020827	2000 model	AC020827 Mus muscu	
c	12	706.4	45.6	249050	1	AL627283	genome 2003	AL627283 Salmonell	
c	13	706.4	45.6	284233	1	AE016849	"	AE016849 Salmonell	
c	14	704.8	45.5	20095	1	AE008909	"	AE008909 Salmonell	
	15	622	40.2	622	6	CQ849497	Appl	CQ849497 Sequence	
	16	612	39.5	612	6	CQ849498		CQ849498 Sequence	
c	17	601	38.8	219912	2	AC020855		AC020855 Mus muscu	
c	18	516.6	33.4	11096	1	AE005656		AE005656 Escherich	
	19	489.8	31.6	1410	1	ECOPYRBIA		K01472 E.coli pyrB	
c	20	463.4	29.9	110000	1	BX950851_04		Continuation (5 of	
c	21	449.8	29.1	51626	2	AC009151		AC009151 Homo sapi	
c	22	413.8	26.7	110000	2	AC073744_1		Continuation (2 of	
	23	405.6	26.2	110000	1	BX936398_41		Continuation (42 o	
	24	402	26.0	10029	1	AE013616		AE013616 Yersinia	
	25	402	26.0	216050	1	AJ414157		AJ414157 Yersinia	
	26	402	26.0	229338	1	AE017142		AE017142 Yersinia	
	27	367.2	23.7	1812	1	STPYRBIG		X05641 S.typhimuri	
	28	367	23.7	1333	1	AF095578		AF095578 Salmonell	
	29	353	22.8	10465	1	AE004321		AE004321 Vibrio ch	
	30	345	22.3	465	6	AR384860		AR384860 Sequence	
c	31	337	21.8	300169	1	AE016801		AE016801 Vibrio vu	
	32	333.8	21.6	248650	1	AP005341		AP005341 Vibrio vu	
	33	317.8	20.5	89934	2	AC008867		AC008867 Homo sapi	
	34	313.4	20.2	387	6	CQ849501		CQ849501 Sequence	
	35	307.4	19.9	349907	1	BX571874		BX571874 Photorhab	
	36	302.2	19.5	1760	1	AF190426		AF190426 Erwinia h	
	37	298.6	19.3	1945	1	SMAPYRBI		J05033 Serratia ma	
c	38	296.8	19.2	4989	1	STU07843		U07843 Salmonella	
	39	292	18.9	423	6	AR384790		AR384790 Sequence	
	40	280.6	18.1	296650	1	AP005082		AP005082 Vibrio pa	
	41	252.6	16.3	1224	6	AR384827		AR384827 Sequence	
c	42	251.8	16.3	2775	6	AR384942		AR384942 Sequence	
	43	219.2	14.2	110000	6	AR409405_3		Continuation (4 of	
	44	219.2	14.2	110000	6	AR409405_4		Continuation (5 of	
	45	219.2	14.2	110000	6	BD061520_3		Continuation (4 of	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 12:14:12 ; Search time 1262 Seconds
(without alignments)
7261.299 Million cell updates/sec

Title: US-10-733-776-1
Perfect score: 1548
Sequence: 1 tcgcgatctggtactgtaag.....tgatcgggtccgaagaagatc 1548

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query						
No.	Score	Match	Length	DB	ID		
1	561.2	36.3	1436	5	AAS93208	2002	Aas93208 DNA encod human
2	462	29.8	462	13	ADT48924	2002 X	Adt48924 Bacterial in plant
3	414	26.7	2913	5	AAS89034	2001	Aas89034 DNA encod human

c	4	414	26.7	2913	5	AAS73466	2002	Aas73466 DNA encod	human
c	5	391	25.3	2697	8	ACA18785	2002	Aca18785 Prokaryot	
c	6	391	25.3	2697	13	ADT48923		Adt48923 Bacterial	
c	7	365	23.6	1267	5	AAS89802		Aas89802 DNA encod	
c	8	365	23.6	1267	5	AAS90167		Aas90167 DNA encod	
c	9	365	23.6	1267	5	AAS89259		Aas89259 DNA encod	
c	10	365	23.6	3678	5	AAS91989		Aas91989 DNA encod	
	11	345	22.3	465	11	ACH95794		Ach95794 Klebsiell	
c	12	330	21.3	3117	5	AAS69095		Aas69095 DNA encod	
c	13	330	21.3	3117	5	AAS89240		Aas89240 DNA encod	
c	14	330	21.3	4942	5	AAS89816		Aas89816 DNA encod	
c	15	330	21.3	4944	5	AAS89273		Aas89273 DNA encod	
c	16	330	21.3	4944	5	AAS90181		Aas90181 DNA encod	
	17	322.4	20.8	2481	5	AAS90282		Aas90282 DNA encod	
c	18	307.4	19.9	110000	10	ACF67367	39	Continuation (40 o	
	19	307.4	19.9	110000	10	ACF65388	08	Continuation (9 of	
c	20	295	19.1	2709	8	ACA51279		Aca51279 Prokaryot	
	21	292	18.9	423	11	ACH95724		Ach95724 Klebsiell	
c	22	291.8	18.9	2709	8	ACA52121		Aca52121 Prokaryot	
c	23	284.8	18.4	1541	8	ACA49041		Aca49041 Prokaryot	
c	24	258.6	16.7	4752	5	AAS89807		Aas89807 DNA encod	
c	25	258.6	16.7	4752	5	AAS89264		Aas89264 DNA encod	
c	26	258.6	16.7	4752	5	AAS73420		Aas73420 DNA encod	
c	27	258.6	16.7	4752	5	AAS94398		Aas94398 DNA encod	
c	28	258.6	16.7	4752	5	AAS90172		Aas90172 DNA encod	
	29	258.6	16.7	4752	5	AAS93795		Aas93795 DNA encod	
c	30	255.8	16.5	2706	8	ACA31992		Aca31992 Prokaryot	
	31	252.6	16.3	1224	11	ACH95761		Ach95761 Klebsiell	
c	32	251.8	16.3	2775	11	ACH95876		Ach95876 Klebsiell	
c	33	251	16.2	2706	8	ACA35909		Aca35909 Prokaryot	
	34	235.8	15.2	465	10	ACF70839		Acf70839 Photorhab	
	35	231.4	14.9	387	10	ACF70838		Acf70838 Photorhab	
	36	225	14.5	1764	5	AAS90169		Aas90169 DNA encod	
	37	225	14.5	1764	5	AAS89261		Aas89261 DNA encod	
	38	225	14.5	1764	5	AAS89804		Aas89804 DNA encod	
	39	224.4	14.5	462	13	ADS45443		Ads45443 Bacterial	
	40	219.2	14.2	110000	6	ABA92787	3	Continuation (4 of	
	41	219.2	14.2	110000	6	ABA92787	4	Continuation (5 of	
	42	207.2	13.4	456	13	ADS45703		Ads45703 Bacterial	
	43	204.4	13.2	393	11	ACH95569		Ach95569 Klebsiell	
	44	204.2	13.2	480	10	ADF01255		Adf01255 Bacterial	
	45	197	12.7	2590	3	AAC79620		Aac79620 Virulence	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 23:18:27 ; Search time 409 Seconds
(without alignments)
6193.047 Million cell updates/sec

Title: US-10-733-776-1
Perfect score: 1548
Sequence: 1 tcgcgatctggtactgtaag.....tgatcgggtccgaagaagatc 1548

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	345	22.3	465	4	US-09-489-039A-1589 2000 Sequence 1589, Ap
2	292	18.9	423	4	US-09-489-039A-1519 " Sequence 1519, Ap
3	252.6	16.3	1224	4	US-09-489-039A-1556 " Sequence 1556, Ap
c 4	251.8	16.3	2775	4	US-09-489-039A-1671 " Sequence 1671, Ap
5	219.2	14.2	640681	4	US-09-790-988-1 " Sequence 1, Appli
6	204.4	13.2	393	4	US-09-489-039A-1364 " Sequence 1364, Ap
7	204.2	13.2	480	4	US-09-543-681A-1540 " Sequence 1540, Ap
8	197	12.7	2590	4	US-09-809-665A-78 " Sequence 78, Appl
9	194.2	12.5	386	4	US-09-809-665A-174 " Sequence 174, App
10	188.2	12.2	1830121	4	US-09-557-884-1 " Sequence 1, Appli
11	188.2	12.2	1830121	4	US-09-643-990A-1 " Sequence 1, Appli

K pneumoniae

c	12	173.4	11.2	2442	4	US-09-328-352-3295	Sequence 3295, Ap
	13	171.4	11.1	402	4	US-09-543-681A-1492	Sequence 1492, Ap
c	14	153.2	9.9	2493	4	US-09-252-991A-10571	Sequence 10571, A
c	15	153.2	9.9	2967	4	US-09-252-991A-10675	Sequence 10675, A
	16	153.2	9.9	3027	4	US-09-252-991A-10492	Sequence 10492, A
c	17	107.8	7.0	1218	4	US-09-252-991A-7267	Sequence 7267, Ap
	18	104.6	6.8	468	4	US-09-252-991A-7435	Sequence 7435, Ap
c	19	98.8	6.4	536165	4	US-09-214-808-1	Sequence 1, Appli
	20	91	5.9	786	4	US-09-489-039A-1447	Sequence 1447, Ap
	21	88.6	5.7	414	4	US-09-543-681A-1634	Sequence 1634, Ap
	22	88.4	5.7	405	4	US-09-134-000C-3050	Sequence 3050, Ap
c	23	85.4	5.5	2858	3	US-09-221-017B-1013	Sequence 1013, Ap
c	24	85.4	5.5	21040	3	US-08-961-527-55	Sequence 55, Appl
	25	83	5.4	456	4	US-09-540-236-881	Sequence 881, App
c	26	81.6	5.3	94750	4	US-09-596-002-38	Sequence 38, Appl
	27	80.6	5.2	402	4	US-09-107-433-1225	Sequence 1225, Ap
c	28	80	5.2	1270	1	US-08-915-003-8	Sequence 8, Appli
c	29	80	5.2	1270	2	US-08-642-247-8	Sequence 8, Appli
	30	78.8	5.1	381	4	US-09-583-110-650	Sequence 650, App
	31	78.8	5.1	4718	4	US-08-956-171E-299	Sequence 299, App
	32	78.8	5.1	4718	4	US-08-781-986A-299	Sequence 299, App
c	33	72.8	4.7	400	3	US-08-976-259-134	Sequence 134, App
c	34	72.8	4.7	400	4	US-09-956-004-134	Sequence 134, App
c	35	72.6	4.7	3466	3	US-09-027-166-10	Sequence 10, Appl
	36	72	4.7	402	3	US-09-134-001C-512	Sequence 512, App
	37	72	4.7	6318	3	US-09-453-702B-230	Sequence 230, App
	38	68.4	4.4	14077	4	US-09-902-540-1109	Sequence 1109, Ap
	39	68	4.4	396	4	US-09-902-540-2456	Sequence 2456, Ap
c	40	66.8	4.3	2667	4	US-09-134-000C-2481	Sequence 2481, Ap
	41	63.4	4.1	2605	3	US-09-651-656-104	Sequence 104, App
	42	63.4	4.1	2605	3	US-09-650-855-104	Sequence 104, App
	43	62.6	4.0	444	4	US-09-328-352-1962	Sequence 1962, Ap
	44	60.2	3.9	1017	3	US-09-125-265-1	Sequence 1, Appli
c	45	58.4	3.8	5629	3	US-09-453-702B-243	Sequence 243, App

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 03:05:23 ; Search time 6575 Seconds
(without alignments)
1443.777 Million cell updates/sec

Title: US-10-733-776-1
Perfect score: 1548
Sequence: 1 tcgcgatctggtactgtaag.....tgatcgggtccgaagaagatc 1548

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				DB	ID	Description
	No.	Score	Match	Length	Query				
	1	1548	100.0	1548	18	US-10-733-776-1	App1		Sequence 1, Appli
c	2	975.6	63.0	1411	18	US-10-733-776-9	"		Sequence 9, Appli
	3	622	40.2	622	18	US-10-733-776-7	"		Sequence 7, Appli
	4	612	39.5	612	18	US-10-733-776-8	"		Sequence 8, Appli
	5	462	29.8	462	17	US-10-369-493-47362	2003 x		Sequence 47362, A
c	6	391	25.3	2697	17	US-10-369-493-47361	"		Sequence 47361, A
c	7	391	25.3	2697	17	US-10-282-122A-6655	2004		Sequence 6655, Ap
	8	313.4	20.2	387	18	US-10-733-776-11	"		Sequence 11, Appl
c	9	295	19.1	2709	17	US-10-282-122A-39149			Sequence 39149, A
c	10	291.8	18.9	2709	17	US-10-282-122A-39991			Sequence 39991, A
c	11	284.8	18.4	1541	17	US-10-282-122A-36911			Sequence 36911, A
c	12	255.8	16.5	2706	17	US-10-282-122A-19862			Sequence 19862, A
c	13	251	16.2	2706	17	US-10-282-122A-23779			Sequence 23779, A
	14	224.4	14.5	462	17	US-10-369-493-23873			Sequence 23873, A
	15	219.2	14.2	640681	9	US-09-790-988-1			Sequence 1, Appli
	16	207.2	13.4	456	17	US-10-369-493-24133			Sequence 24133, A
	17	197	12.7	2590	11	US-09-809-665A-78			Sequence 78, Appl
	18	197	12.7	2590	18	US-10-854-299-78			Sequence 78, Appl
	19	194.2	12.5	386	11	US-09-809-665A-174			Sequence 174, App
	20	194.2	12.5	386	18	US-10-854-299-174			Sequence 174, App
c	21	188.4	12.2	2514	17	US-10-369-493-37708			Sequence 37708, A
	22	188.2	12.2	1830121	17	US-10-329-670-1			Sequence 1, Appli
	23	188.2	12.2	1830121	18	US-10-158-865-1			Sequence 1, Appli
c	24	170.4	11.0	2754	17	US-10-282-122A-8510			Sequence 8510, Ap
	25	163.8	10.6	597	18	US-10-363-345A-10927			Sequence 10927, A
c	26	163.8	10.6	597	18	US-10-363-345A-10928			Sequence 10928, A
	27	163.8	10.6	597	19	US-10-363-483A-10927			Sequence 10927, A
c	28	163.8	10.6	597	19	US-10-363-483A-10928			Sequence 10928, A
c	29	162.6	10.5	597	18	US-10-363-345A-10925			Sequence 10925, A
	30	162.6	10.5	597	18	US-10-363-345A-10926			Sequence 10926, A
c	31	162.6	10.5	597	19	US-10-363-483A-10925			Sequence 10925, A
	32	162.6	10.5	597	19	US-10-363-483A-10926			Sequence 10926, A
c	33	153.2	9.9	2712	17	US-10-282-122A-30551			Sequence 30551, A
c	34	146.8	9.5	2760	17	US-10-282-122A-32143			Sequence 32143, A
c	35	138.6	9.0	2649	17	US-10-282-122A-12198			Sequence 12198, A
c	36	134	8.7	2700	17	US-10-282-122A-41612			Sequence 41612, A
c	37	128.8	8.3	684707	17	US-10-398-221-9			Sequence 9, Appli
	38	128.8	8.3	3011208	17	US-10-398-221-2058			Sequence 2058, Ap
c	39	126.8	8.2	2571	17	US-10-282-122A-24506			Sequence 24506, A
c	40	120.4	7.8	5101	17	US-10-398-221-3829			Sequence 3829, Ap
c	41	120	7.8	2643	17	US-10-282-122A-16514			Sequence 16514, A
	42	117	7.6	117	17	US-10-339-674-3370			Sequence 3370, Ap
c	43	112	7.2	112	17	US-10-339-674-3371			Sequence 3371, Ap
	44	107.6	7.0	378	9	US-09-974-300-1229			Sequence 1229, Ap
c	45	103.8	6.7	639	17	US-10-264-237-333			Sequence 333, App

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 21:25:17 ; Search time 7780 Seconds
(without alignments)
7573.713 Million cell updates/sec

Title: US-10-733-776-1
Perfect score: 1548
Sequence: 1 tcgcgatctggtactgtaag.....tgatcgggtccgaagaagatc 1548

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query				ID	Description
	No.	Score	Match	Length	DB	DB	DB	DB		
c	1	821.4	53.1	847	9	CL684250	2004		CL684250	PRI0139a_
	2	776.8	50.2	812	9	CL666243	"		CL666243	PRI0151d_
	3	775	50.1	807	9	CL666063	"		CL666063	PRI0151b_
c	4	210.2	13.6	226	4	BG382346	low low		BG382346	298212 MA
c	5	191.2	12.4	752	9	CL658545			CL658545	PRI0131d_
c	6	188.8	12.2	815	9	CL693441			CL693441	PRI0161c_
c	7	177.8	11.5	837	9	CL674143			CL674143	PRI0111b_
	8	168.8	10.9	2376	9	CL982206			CL982206	OsIFSC046

c	9	167.6	10.8	2952	9	CL982245	CL982245	OsIFSC047
	10	151	9.8	780	7	CN586720	CN586720	USDA-FP_1
	11	133.6	8.6	1338	8	BZ578038	BZ578038	msh2_569.
	12	126	8.1	371	8	BH404705	BH404705	AG-ND-120
	13	125.6	8.1	397	2	AW983564	AW983564	RC3-HN000
c	14	104.6	6.8	828	9	CL653278	CL653278	PRI0118a_
	15	101.4	6.6	103	8	BH828707	BH828707	BACPP28-I
c	16	100	6.5	545	4	BJ619265	BJ619265	BJ619265
c	17	100	6.5	578	4	BJ619554	BJ619554	BJ619554
c	18	99.6	6.4	764	9	CL661098	CL661098	PRI0138d_
	19	98.6	6.4	725	4	BJ446039	BJ446039	BJ446039
	20	98.6	6.4	726	4	BJ437530	BJ437530	BJ437530
	21	98.2	6.3	543	4	BJ440775	BJ440775	BJ440775
	22	97.6	6.3	706	4	BJ436835	BJ436835	BJ436835
c	23	97.6	6.3	723	6	C92149	C92149	C92149 Dict
	24	97	6.3	614	4	BJ434606	BJ434606	BJ434606
c	25	95.4	6.2	794	9	CL666059	CL666059	PRI0151b_
	26	95.2	6.1	549	1	AI857022	AI857022	MBNaAd-11
	27	95.2	6.1	805	9	CL668572	CL668572	PRI0158a_
c	28	95	6.1	1222	8	BZ572121	BZ572121	msh2_2521
c	29	94.8	6.1	1178	8	BZ563590	BZ563590	pacs2-164
	30	94.4	6.1	411	1	AI986973	AI986973	rs20b03.y
	31	94.4	6.1	665	4	BJ096681	BJ096681	BJ096681
	32	94.4	6.1	692	4	BJ614351	BJ614351	BJ614351
	33	94.4	6.1	698	4	BJ615952	BJ615952	BJ615952
	34	94.2	6.1	705	5	BU725610	BU725610	SJMCFH11
	35	93	6.0	745	9	CL683470	CL683470	PRI0137a_
	36	92.8	6.0	585	7	CO250307	CO250307	WS00810.B
c	37	92.6	6.0	846	9	CL693676	CL693676	PRI0162b_
	38	92.6	6.0	868	7	CK864671	CK864671	AGENCOURT
	39	92.6	6.0	1258	9	CG754091	CG754091	P049-2-F0
	40	92.6	6.0	1372	9	CG749233	CG749233	P043-2-F0
c	41	92.2	6.0	649	7	CF322664	CF322664	HDN--01-L
c	42	91.8	5.9	672	4	BJ787914	BJ787914	BJ787914
	43	91.6	5.9	498	1	AT006939	AT006939	AT006939
	44	91.4	5.9	490	4	BJ757406	BJ757406	BJ757406
	45	91.4	5.9	502	4	BM279297	BM279297	Nb_ad1_05